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RAW SEQUENCE LISTING

DATE: 02/11/2002

PATENT APPLICATION: US/09/772,134B

TIME: 14:30:53

Input Set : A:\EP.txt

Output Set: N:\CRF3\02112002\I772134B.raw

p5

3 <110> APPLICANT: Southern Illinois University
 4 Lightfoot, David
 5 Meksem, Khalid
 7 <120> TITLE OF INVENTION: ISOLATED POLYNUCLEOTIDES AND POLYPEPTIDES RELATING TO LOCI
 UNDERLYING
 8 RESISTANCE TO SOYBEAN CYST NEMATODE AND SOYBEAN SUDDEN DEATH SYNDROME AND
 9 METHODS EMPLOYING SAME
 11 <130> FILE REFERENCE: 1268/4/2
 13 <140> CURRENT APPLICATION NUMBER: 09/772,134B
 14 <141> CURRENT FILING DATE: 2001-01-29
 16 <150> PRIOR APPLICATION NUMBER: 60/178,811
 17 <151> PRIOR FILING DATE: 2000-01-28
 19 <160> NUMBER OF SEQ ID NOS: 122
 21 <170> SOFTWARE: PatentIn version 3.0
 23 <210> SEQ ID NO: 1
 24 <211> LENGTH: 87
 25 <212> TYPE: DNA
 26 <213> ORGANISM: soybean
 28 <400> SEQUENCE: 1
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 31 tgggtttctg ataaccgtgg tcgttaa 87
 34 <210> SEQ ID NO: 2
 35 <211> LENGTH: 92
 36 <212> TYPE: DNA
 37 <213> ORGANISM: soybean
 39 <400> SEQUENCE: 2
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 42 agatttgggt ttcagataac cgtggtcgtt aa 92
 45 <210> SEQ ID NO: 3
 46 <211> LENGTH: 113
 47 <212> TYPE: DNA
 48 <213> ORGANISM: soybean
 50 <400> SEQUENCE: 3
 51 gaattcctaa tatacgagtg aatattattg taatgcttgt aaaaaaacat gataaaatgc 60
 53 aaaaatttgg ggtgaatttt tacgacatta gtgaaaaaaa catatccctt taa 113
 56 <210> SEQ ID NO: 4
 57 <211> LENGTH: 135
 58 <212> TYPE: DNA
 59 <213> ORGANISM: soybean
 61 <400> SEQUENCE: 4
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 64 ttgaaaaaa tgtactagat atatcatggt tttttacaag cattacaata atattcactc 120
 66 gtatattagg aattc 135
 69 <210> SEQ ID NO: 5

ENTERED

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71 <212> TYPE: DNA
72 <213> ORGANISM: soybean
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77 caggctttga gaggcataga aataattttt ttatataaaa aaaaagtctt ctttaa      116
80 <210> SEQ ID NO: 6
81 <211> LENGTH: 113
82 <212> TYPE: DNA
83 <213> ORGANISM: soybean
85 <400> SEQUENCE: 6
86 gaatttcggt tatctcagac aacttttggt tggtttggtt atagtaaaga cacgattatc      60
88 caggctttga gaggcataga aataattttt ttatataaaa aaaagtctct tta      113
91 <210> SEQ ID NO: 7
92 <211> LENGTH: 409
93 <212> TYPE: DNA
94 <213> ORGANISM: soybean - Forrest
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99 gcaaacgata atataattat aagaaaaaga cacactttga gggcattttt gacttgagag      120
101 aactcaggta tcaatctaaa agcaacgctg ttcaccttga gctgaaacac ctggaggaga      180
103 aagcaaagca aaccaaacgc gagagagaaa taaagaacgg aaacagagag agagagagga      240
105 aggaccttgt tcaaagcaac ggggacaact ttagagccct ggcgcgcgtg ggggtcaata      300
107 agcgtaacct ggctgaggag agcctcggcg tcgtccttgc tgaagcagaa gaggaagagc      360
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112 <210> SEQ ID NO: 8
113 <211> LENGTH: 417
114 <212> TYPE: DNA
115 <213> ORGANISM: soybean
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120 actaaaatat ttgcaaagca taatataatt ataagaaaaa gactcacttt gagggcattt      120
122 ttgacttgag agaactcagg tatcaatcta aaagcaacgc tggtcacctt gagctgaaac      180
124 acctggagga gaaagcaaag caaaccaaac gcgagagaga aataaagaac ggaaacagag      240
126 agagaggaag gaccttggtc aaagcaacgg ggacaacttt agagccctgg cgcgcgtggg      300
128 ggtcaataag cgtaacctgg ctgaggagag cctcggcgcc gtccttgctg aagcagaaga      360
130 ggaagagccc gagaccaaga gaaactcctc ggaagcaacg ggaatttgta cgcagtc      417
133 <210> SEQ ID NO: 9
134 <211> LENGTH: 165
135 <212> TYPE: DNA
136 <213> ORGANISM: soybean
138 <400> SEQUENCE: 9
139 gagtaaatga aaatcgatca aaatcaaata atatatgctt tttttagttg tgttcaagta      60
141 actttttttt attgaaaaaa tcgacccaag ttgaaacaca tgtttgagaa ttgttttggt      120
143 catccaacgt ttttcttgta caatcagctg tgagagggga attgg      165
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147 <211> LENGTH: 164
148 <212> TYPE: DNA
149 <213> ORGANISM: soybean

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151 <400> SEQUENCE: 10
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154 ctttttttta ttgaaaaaat cgacccaagt tgaaacacat gtttgagaat tgttttgtgc      120
156 atccaacggt tttcttgtac aatcagctgt gagaggggaa ttgg      164
159 <210> SEQ ID NO: 11
160 <211> LENGTH: 114
161 <212> TYPE: DNA
162 <213> ORGANISM: soybean
164 <400> SEQUENCE: 11
165 gaattcccag ctagatttgt atcaaacatg tattgtccac aaaatgttca agcatcttag      60
167 ggaactgcta ttcttacttc taaatttttt attgacatcc aaagtgtgct ttaa      114
170 <210> SEQ ID NO: 12
171 <211> LENGTH: 114
172 <212> TYPE: DNA
173 <213> ORGANISM: soybean
175 <400> SEQUENCE: 12
176 gaattcccag ccagatttgt atcaaacatg tattgtccac aaaatgttca agcatcttag      60
178 ggaactgcta ttcttacttc taaatttttt attgacatcc aaagtgtgct ttaa      114
181 <210> SEQ ID NO: 13
182 <211> LENGTH: 3106
183 <212> TYPE: DNA
184 <213> ORGANISM: soybean
186 <220> FEATURE:
187 <221> NAME/KEY: misc_feature
188 <222> LOCATION: (1)..(3106)
189 <223> OTHER INFORMATION: n is an undetermined nucleotide (dATP, dCTP, dGTP, or dTTP)
192 <400> SEQUENCE: 13
193 aatgggagga gtgggaaaga cagtggctat ggagcttggt cggagggttg ggttggaatc      60
195 aagtgtgctc agggacaggt tattgtgac cagcttcctt ggaagggttt gaggggtcga      120
197 atcacgcaca aaattggcca acttcaaggc ctcaggaagc ttagtcttca tgataaccaa      180
199 attggtggtt caatcccttc aactttggga cttcttccca accttagagg ggttcagtta      240
201 ttcaacaata ggcttacagg ttccatacct ctttcttttag gtttctgcct ttgcttcaag      300
203 tctcttgacc tcagcaacaa cttgttcaca ggagcaatcc cttatagtct tgctaattcc      360
205 actaagcttt attggcttaa cttgagtttc aactccttct ctggtccttt accagctagc      420
207 ctaactcact cattttctct cacttttctt tctcttcaaa ataacaatct ttctggctcc      480
209 cttoctaact cttgggggtg gaattccaag aatggcttct ttaggcttca aaatttgatc      540
211 ctagatcata actttttcac tggtagcgtt cctgcttctt tgggtagctt aagagagctc      600
213 aatgagattt cccttagtca taataagttt agtggagcta taccaaatga aataggaacc      660
215 ctttctaggc ttaagacact tgacatttct aataatgcct tgaatgggaa cttgcctgct      720
217 accctctcta atttatcctc acttacactg ctgaatgcag agaacaacct ccttgacaat      780
219 caaatccctc aaagtttagg tagattgcgt aatctttctg ttctgatttt gagtagaaac      840
221 caatttagtg gacatatcc ttcaagcatt gcaaacattt cctcgcttag gcagcttgat      900
223 ttgtcaactga ataatttcag tggagaaatt ccagtctcct ttgacagtca gcgcagtcta      960
225 aatctcttca atgtttccta caatagcctc tcagggttctg tccccctct gcttgccaag      1020
227 aaatttaact caagctcatt tgtgggaaat attcaactat gtgggtacag cccttcaacc      1080
229 ccattgtctt cccaagctcc atcacaagga gtcattgcc cacctcctga agtgtcaaaa      1140
231 catcaccatc ataggaagct aagcaccaaa gacataattc tcatagtagc aggagttctc      1200
233 ctogtagtcc tgattatact ttgttgtgtc ctgcttttct gcctgatcag aaagagatca      1260
235 acatctaggc cgggaacggc caagccaccc gagggtagag cggccactat gaggacagaa      1320

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237 aaaggagtcc ctccagttgc tgggtggtgat gttgaagcag gtggggaggc tggagggaaa 1380
239 ctagtccatt ttgatggacc aatggctttt acagctgatg atctcttggtg tgcaacagct 1440
241 gagatcatgg gaaagagcac ctatggaact gtttataagg ctatttttga ggatggaagt 1500
243 caagttgcag taaagagatt gagggaaaag atcactaaag gtcatagaga atttgaatca 1560
245 gaagtcagtg ttctaggaaa aattagacac cccaatgttt tggctctgag ggcctattac 1620
247 ttgggaccca aaggggaaaa gcttctgggt tttgatacat gtctaaagga agtcttgctt 1680
249 ctttctctca tgggaaggttc gtgtgctggt tctttcatta aagtgtttgtg tgtgctggtc 1740
251 ttttaattata atttgaggtt ttaccttagt aatctgtata attotaatcg gagaacagta 1800
W--> 253 caaacaaaaa cacctaagga acaacacctt anctttaata taccatatca ataaagtga 1860
255 atattttctt ggtcatcttg atgcaggggg aactgaacat tcattattgg ccacaagatt 1920
257 aaaatagccc aagccttgge cggggttgtt ttgccttcat tcccaggaga acatcataca 1980
W--> 259 tgggacctcn catccagcaa tgtgtggctt gatgaaaaac aaatgctaaa attcagattt 2040
261 tggctctttt cgggttgatg tcaactgctg ctaattccaa cgtgatagct acagctggag 2100
263 cattggatac cgggcacctg agctctcaaa gctcaagaaa gcaaacta aaactgatat 2160
265 ctacagtctt ggtgttatct tgttagaact cctaacgagg aaatcacctg ggggtgtctat 2220
267 gaatggacta gatttgcttc agtgggttgc ctacagttgtc aaagaggagt ggacaaatga 2280
269 ggtttttgat gcagacttga tgagagatgc atccacagtt ggcgacgagt tgctaaacac 2340
271 gttgaagctc gctttgcact gtgttgatcc ttctccatca gcacgaccag aagttcatca 2400
273 agttctccag cagctgaaga gattagacca gagagatcag tcacagccag tcccggggac 2460
275 gatatcgtat agcacaaatt ttgcattgat ttttttgtgc caaatgtagt aggcctacta 2520
277 tatatatgtt ctatgattct ttcattctta tattattttt gcctgtttga atgcttgaat 2580
279 ttgtacatac tcatactaca ataagggtga gttctggtta attttacctc tacctcaaa 2640
281 ctgggggtga attctgttct ctccaaggca cataatagtt gaaaatagtt ctcaggagca 2700
283 ttcatgtgtt attctgcaag attctcttct acggctgcta tcttctatgc atgccctgcc 2760
285 cataaatgca ttatgaagaa ttgtaacggc tgtgtttttg gaotttctca aaaagtttat 2820
287 gttattgcca ggtgtatata tcaacatgtt ttaaagattt tcaaacaatc aggttttaga 2880
289 tgtgggtttg catgcatgag attggactag tgcgcttgat gtagtataaa atataaattg 2940
291 tccaatcaag caccctctac atgtccaaat aatgggcctt atgaaactta attttttaat 3000
W--> 293 tacaactac agtaatcttt ttgaataaag atttacaat tacaacngac atgtgaagcn 3060
W--> 295 gcattctttna ttgncaatct ttcaagttac tctattattt tctgcn 3106
298 <210> SEQ ID NO: 14
299 <211> LENGTH: 830
300 <212> TYPE: PRT
301 <213> ORGANISM: soybean
303 <220> FEATURE:
304 <221> NAME/KEY: misc_feature
305 <222> LOCATION: (1)..(830)
306 <223> OTHER INFORMATION: Xaa is any amino acid
309 <400> SEQUENCE: 14
311 Asn Gly Arg Ser Gly Lys Asp Ser Gly Tyr Gly Ala Cys Ser Gly Gly
312 1 5 10 15
314 Trp Val Gly Ile Lys Cys Ala Gln Gly Gln Val Ile Val Ile Gln Leu
315 20 25 30
317 Pro Trp Lys Gly Leu Arg Gly Arg Ile Thr Asp Lys Ile Gly Gln Leu
318 35 40 45
320 Gln Gly Leu Arg Lys Leu Ser Leu His Asp Asn Gln Ile Gly Gly Ser
321 50 55 60
323 Ile Pro Ser Thr Leu Gly Leu Leu Pro Asn Leu Arg Gly Val Gln Leu
324 65 70 75 80

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326 Phe Asn Asn Arg Leu Thr Gly Ser Ile Pro Leu Ser Leu Gly Phe Cys
327      85      90      95
329 Pro Leu Leu Gln Ser Leu Asp Leu Ser Asn Asn Leu Leu Thr Gly Ala
330      100      105      110
332 Ile Pro Tyr Ser Leu Ala Asn Ser Thr Lys Leu Tyr Trp Leu Asn Leu
333      115      120      125
335 Ser Phe Asn Ser Phe Ser Gly Pro Leu Pro Ala Ser Leu Thr His Ser
336      130      135      140
338 Phe Ser Leu Thr Phe Leu Ser Leu Gln Asn Asn Asn Leu Ser Gly Ser
339 145      150      155      160
341 Leu Pro Asn Ser Trp Gly Gly Asn Ser Lys Asn Gly Phe Phe Arg Leu
342      165      170      175
344 Gln Asn Leu Ile Leu Asp His Asn Phe Phe Thr Gly Asp Val Pro Ala
345      180      185      190
347 Ser Leu Gly Ser Leu Arg Glu Leu Asn Glu Ile Ser Leu Ser His Asn
348      195      200      205
350 Lys Phe Ser Gly Ala Ile Pro Asn Glu Ile Gly Thr Leu Ser Arg Leu
351      210      215      220
353 Lys Thr Leu Asp Ile Ser Asn Asn Ala Leu Asn Gly Asn Leu Pro Ala
354 225      230      235      240
356 Thr Leu Ser Asn Leu Ser Ser Leu Thr Leu Asn Ala Glu Asn Asn
357      245      250      255
359 Leu Leu Asp Asn Gln Ile Pro Gln Ser Leu Gly Arg Leu Arg Asn Leu
360      260      265      270
362 Ser Val Leu Ile Leu Ser Arg Asn Gln Phe Ser Gly His Ile Pro Ser
363      275      280      285
365 Ser Ile Ala Asn Ile Ser Ser Leu Arg Gln Leu Asp Leu Ser Leu Asn
366      290      295      300
368 Asn Phe Ser Gly Glu Ile Pro Val Ser Phe Asp Ser Gln Arg Ser Leu
369 305      310      315      320
371 Asn Leu Ser Asn Val Ser Tyr Asn Ser Leu Ser Gly Ser Val Pro Pro
372      325      330      335
374 Leu Leu Ala Lys Lys Phe Asn Ser Ser Ser Phe Val Gly Asn Ile Gln
375      340      345      350
377 Leu Cys Gly Tyr Ser Pro Ser Thr Pro Cys Leu Ser Gln Ala Pro Ser
378      355      360      365
380 Gln Gly Val Ile Ala Pro Pro Glu Val Ser Lys His His His His
381      370      375      380
383 Arg Lys Leu Ser Thr Lys Asp Ile Ile Leu Ile Val Ala Gly Val Leu
384 385      390      395      400
386 Leu Val Val Leu Ile Ile Leu Cys Cys Val Leu Leu Phe Cys Leu Ile
387      405      410      415
389 Arg Lys Arg Ser Thr Ser Lys Ala Gly Asn Gly Gln Ala Thr Glu Gly
390      420      425      430
392 Arg Ala Ala Thr Met Arg Thr Glu Lys Gly Val Pro Pro Val Ala Gly
393      435      440      445
395 Gly Asp Val Glu Ala Gly Gly Glu Ala Gly Gly Lys Leu Val His Phe
396      450      455      460
398 Asp Gly Pro Met Ala Phe Thr Ala Asp Asp Leu Leu Cys Ala Thr Ala

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Use of n and/or Xaa has been detected in the Sequence Listing.
 Review the Sequence Listing to insure a corresponding
 explanation is presented in the <220> to <223> fields of
 each sequence using n or Xaa.

VERIFICATION SUMMARY

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L:259 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:13
L:293 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:13
L:295 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:13
L:425 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:14
L:428 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:14
L:431 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:14
L:434 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:14
L:440 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:14
L:443 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:14
L:452 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:14
L:458 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:14
L:461 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:14
L:473 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:15
L:481 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:15
L:493 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:15
L:499 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:15
L:501 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:15
L:503 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:15
L:512 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:16
L:538 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:16
L:547 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:17
L:553 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:17
L:555 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:17
L:557 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:17
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L:565 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:17
L:567 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:17
L:569 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:17
L:571 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:17
L:580 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:18
L:602 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:18
L:604 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:18
L:606 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:18
L:608 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:18
L:610 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:18
L:621 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:19
L:639 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:19
L:643 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:19
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L:647 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:19
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L:651 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:19
L:690 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:20
L:692 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:20
L:694 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:20

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L:727 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:21
L:729 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:21
L:731 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:21
L:733 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:21
L:735 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:21
L:2035 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:58
L:2047 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:58
L:2049 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:58